

OIPE

#13

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/864,291

DATE: 12/11/2001
 TIME: 15:07:44

Input Set : A:\1669 0050001 seq list.txt
 Output Set: N:\CRF3\12112001\I864291.raw

ENTERED

5 <110> APPLICANT: Oko, Richard
 7 Sutovsky, Peter
 11 <120> TITLE OF INVENTION: PT32 Sperm Protein, Sperm c-Yes, Oocyte Cytoplasmic c-Yes,
 and Uses

12 Thereof
 16 <130> FILE REFERENCE: 1669.0050001
 20 <140> CURRENT APPLICATION NUMBER: US 09/864,291
 22 <141> CURRENT FILING DATE: 2001-05-25
 26 <150> PRIOR APPLICATION NUMBER: US 60/206,979
 28 <151> PRIOR FILING DATE: 2000-05-25
 32 <150> PRIOR APPLICATION NUMBER: CA 2,307,128
 34 <151> PRIOR FILING DATE: 2000-05-25
 38 <160> NUMBER OF SEQ ID NOS: 20
 42 <170> SOFTWARE: PatentIn version 3.1
 46 <210> SEQ ID NO: 1
 48 <211> LENGTH: 5
 50 <212> TYPE: PRT
 52 <213> ORGANISM: mammalian
 56 <400> SEQUENCE: 1
 58 Pro Pro Pro Gly Tyr
 59 1 5
 62 <210> SEQ ID NO: 2
 64 <211> LENGTH: 5
 66 <212> TYPE: PRT
 68 <213> ORGANISM: mammalian
 72 <400> SEQUENCE: 2
 74 Leu Pro Pro Ala Tyr
 75 1 5
 78 <210> SEQ ID NO: 3
 80 <211> LENGTH: 7
 82 <212> TYPE: PRT
 84 <213> ORGANISM: mammalian
 88 <220> FEATURE:
 90 <221> NAME/KEY: misc_feature
 92 <222> LOCATION: (3)..(3)
 94 <223> OTHER INFORMATION: X may be any amino acid residue
 98 <220> FEATURE:
 100 <221> NAME/KEY: misc_feature
 102 <222> LOCATION: (6)..(6)
 104 <223> OTHER INFORMATION: X may be any amino acid residue
 108 <400> SEQUENCE: 3
 W--> 110 Tyr Gly Xaa Pro Pro Xaa Gly
 111 1 5
 114 <210> SEQ ID NO: 4
 116 <211> LENGTH: 1413
 118 <212> TYPE: DNA
 120 <213> ORGANISM: mammalian
 124 <220> FEATURE:

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126 <221> NAME/KEY: CDS
128 <222> LOCATION: (36)..(974)
130 <223> OTHER INFORMATION:
134 <400> SEQUENCE: 4
135 cggcacgagg ggcggcagga gggggcctgg gcagg atg gca gtg aac cag agc      53
136                               Met Ala Val Asn Gln Ser
137                               1           5
139 cac acc gag agc cgt cgt ggg gcc ctc atc ccc tct ggc gaa agt gtc      101
140 His Thr Glu Ser Arg Arg Gly Ala Leu Ile Pro Ser Gly Glu Ser Val
141                               10           15           20
143 ttg aag cag tgt gag gat gtg gac ctc tgc ttc cta cag aaa cca gtg      149
144 Leu Lys Gln Cys Glu Asp Val Asp Leu Cys Phe Leu Gln Lys Pro Val
145                               25           30           35
147 gaa tcc tat ctc ttt aat ggc aca aag aaa gga acg ttg ttt ctc act      197
148 Glu Ser Tyr Leu Phe Asn Gly Thr Lys Lys Gly Thr Leu Phe Leu Thr
149                               40           45           50
151 tca tac cgg gtg gtc ttc gtg act tca cac tta gtc aat gac ccc atg      245
152 Ser Tyr Arg Val Val Phe Val Thr Ser His Leu Val Asn Asp Pro Met
153 55                               60           65           70
155 ctt tct ttt atg atg ccg ttt ggc ctg atg agt gac tgc acc att gaa      293
156 Leu Ser Phe Met Met Pro Phe Gly Leu Met Ser Asp Cys Thr Ile Glu
157                               75           80           85
159 caa cca att ttt gcc ccc aac tac att aaa gga acc att cag gca gct      341
160 Gln Pro Ile Phe Ala Pro Asn Tyr Ile Lys Gly Thr Ile Gln Ala Ala
161                               90           95           100
163 cca ggt ggt ggc tgg gaa gga caa gct gtt ttt aag tta tcc ttc agg      389
164 Pro Gly Gly Gly Trp Glu Gly Gln Ala Val Phe Lys Leu Ser Phe Arg
165                               105          110          115
167 aaa gga ggt gcc atc gaa ttt gcc caa ctg atg gta aaa gct gcc tct      437
168 Lys Gly Gly Ala Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser
169                               120          125          130
171 gct gct gcc aga gga att cca ctt gga agt gta aat tac tgg ttc gac      485
172 Ala Ala Ala Arg Gly Ile Pro Leu Gly Ser Val Asn Tyr Trp Phe Asp
173 135                               140          145          150
175 act tca gga ctg tac ata att act gtc cca ggg gct gca gtg tgc tcc      533
176 Thr Ser Gly Leu Tyr Ile Ile Thr Val Pro Gly Ala Ala Val Cys Ser
177                               155          160          165
179 tca cag aca cct tgt cca gca tat cca att gtg atc tat gga ccc cca      581
180 Ser Gln Thr Pro Cys Pro Ala Tyr Pro Ile Val Ile Tyr Gly Pro Pro
181                               170          175          180
183 cca cca gga tat aca gtc caa cca ggg gaa tat gga act cca cca gaa      629
184 Pro Pro Gly Tyr Thr Val Gln Pro Gly Glu Tyr Gly Thr Pro Pro Glu
185                               185          190          195
187 gga tat gga gcc caa cca ggg gga tat gga gcc cca cct atg gga tat      677
188 Gly Tyr Gly Ala Gln Pro Gly Gly Tyr Gly Ala Pro Pro Met Gly Tyr
189                               200          205          210
191 gga gcc ccg cct gtg gga tat gga gtc cca cct ggg gga tat gga gtc      725
192 Gly Ala Pro Pro Val Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val
193 215                               220          225          230

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195 cca cct ggg gga tat gga gtc cca cct ggg gga tat gga gcc cca cct      773
196 Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro
197                               235                               240                               245
199 ggg gga tat gga gtc cca cct ggg gga tat ggt gcc cca cct ggg gga      821
200 Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly
201                               250                               255                               260
203 tat gga gcc cca cct gca gga tat gga gcc cca cca gct gga aat gaa      869
204 Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Ala Gly Asn Glu
205                               265                               270                               275
207 gcc cta ccc cct gca tat gaa gct cca tct gct gga aat aca gct gcc      917
208 Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr Ala Ala
209                               280                               285                               290
211 tct cac aga tct atg aca gct cag cag gag act tct ctt ccc act acc      965
212 Ser His Arg Ser Met Thr Ala Gln Gln Glu Thr Ser Leu Pro Thr Thr
213 295                               300                               305                               310
215 tca tct tct taggtccatt taccaccttc tcagagttaa accttgaaga      1014
216 Ser Ser Ser
219 ctcaccaagc aaagggcacc ctaaaaactga agtcacagta agaaggaaga cccaggtgcc      1074
221 cagtggtagg aggtgttcgt gtgcacgcag tgggtctgac ttctccacac acctgtgagg      1134
223 tctgtgcct caaaacagat gaaggtgaga agacgactcc tgttctcaag gaaggaagat      1194
225 gcttgaaaac agactgcaag ccaactagag agagagagat gtgaagtggc acataaaaca      1254
227 gcttggggat ggagactgac tctctttaga aaacaggcct tctccctgcc tctgacctga      1314
229 gcagaaaaga gaaatcgctg gaaccaaaga gctaggggtca cctgtcttag acgccctcga      1374
231 ttaaagcctg cttgctgttg cataaaaaaa aaaaaaaaaa      1413
234 <210> SEQ ID NO: 5
236 <211> LENGTH: 313
238 <212> TYPE: PRT
240 <213> ORGANISM: mammalian
244 <400> SEQUENCE: 5
246 Met Ala Val Asn Gln Ser His Thr Glu Ser Arg Arg Gly Ala Leu Ile
247 1                               5                               10                               15
250 Pro Ser Gly Glu Ser Val Leu Lys Gln Cys Glu Asp Val Asp Leu Cys
251                               20                               25                               30
254 Phe Leu Gln Lys Pro Val Glu Ser Tyr Leu Phe Asn Gly Thr Lys Lys
255                               35                               40                               45
258 Gly Thr Leu Phe Leu Thr Ser Tyr Arg Val Val Phe Val Thr Ser His
259                               50                               55                               60
262 Leu Val Asn Asp Pro Met Leu Ser Phe Met Met Pro Phe Gly Leu Met
263 65                               70                               75                               80
266 Ser Asp Cys Thr Ile Glu Gln Pro Ile Phe Ala Pro Asn Tyr Ile Lys
267                               85                               90                               95
270 Gly Thr Ile Gln Ala Ala Pro Gly Gly Gly Trp Glu Gly Gln Ala Val
271                               100                              105                              110
274 Phe Lys Leu Ser Phe Arg Lys Gly Gly Ala Ile Glu Phe Ala Gln Leu
275                               115                              120                              125
278 Met Val Lys Ala Ala Ser Ala Ala Ala Arg Gly Ile Pro Leu Gly Ser
279                               130                              135                              140
282 Val Asn Tyr Trp Phe Asp Thr Ser Gly Leu Tyr Ile Ile Thr Val Pro
283 145                               150                              155                              160

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286 Gly Ala Ala Val Cys Ser Ser Gln Thr Pro Cys Pro Ala Tyr Pro Ile
287                               165                               170
290 Val Ile Tyr Gly Pro Pro Pro Pro Gly Tyr Thr Val Gln Pro Gly Glu
291                               180                               185
294 Tyr Gly Thr Pro Pro Glu Gly Tyr Gly Ala Gln Pro Gly Gly Tyr Gly
295                               195                               200
298 Ala Pro Pro Met Gly Tyr Gly Ala Pro Pro Val Gly Tyr Gly Val Pro
299                               210                               215
302 Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly
303 225                               230                               235
306 Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr
307                               245                               250
310 Gly Ala Pro Pro Gly Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala
311                               260                               265
314 Pro Pro Ala Gly Asn Glu Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser
315                               275                               280
318 Ala Gly Asn Thr Ala Ala Ser His Arg Ser Met Thr Ala Gln Gln Glu
319                               290                               295
322 Thr Ser Leu Pro Thr Thr Ser Ser Ser
323 305                               310

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326 <210> SEQ ID NO: 6

328 <211> LENGTH: 24

330 <212> TYPE: PRT

332 <213> ORGANISM: mammalian

336 <400> SEQUENCE: 6

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338 Thr Ser Tyr Arg Val Val Phe Val Thr Ser His Leu Val Asn Asp Pro
339 1                               5                               10                               15

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342 Met Leu Ser Phe Met Met Pro Phe
343                               20

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346 <210> SEQ ID NO: 7

348 <211> LENGTH: 16

350 <212> TYPE: PRT

352 <213> ORGANISM: mammalian

356 <400> SEQUENCE: 7

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358 Asn Glu Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr
359 1                               5                               10                               15

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362 <210> SEQ ID NO: 8

364 <211> LENGTH: 4

366 <212> TYPE: PRT

368 <213> ORGANISM: mammalian

372 <220> FEATURE:

374 <221> NAME/KEY: misc_feature

376 <222> LOCATION: (3)..(3)

378 <223> OTHER INFORMATION: X may be any amino acid

382 <400> SEQUENCE: 8

W--> 384 Pro Pro Xaa Tyr

385 1

388 <210> SEQ ID NO: 9

390 <211> LENGTH: 239

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Input Set : A:\1669 0050001 seq list.txt

Output Set: N:\CRF3\12112001\I864291.raw

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392 <212> TYPE: PRT
394 <213> ORGANISM: Bos sp.
398 <400> SEQUENCE: 9
400 Met Pro Phe Gly Leu Met Ser Asp Cys Thr Ile Glu Gln Pro Ile Phe
401 1 5 10 15
404 Ala Pro Asn Tyr Ile Lys Gly Thr Ile Gln Ala Ala Pro Gly Gly Gly
405 20 25 30
408 Trp Glu Gly Gln Ala Val Phe Lys Leu Ser Phe Arg Lys Gly Gly Ala
409 35 40 45
412 Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Ala Ala Arg
413 50 55 60
416 Gly Ile Pro Leu Gly Ser Val Asn Tyr Trp Phe Asp Thr Ser Gly Leu
417 65 70 75 80
420 Tyr Ile Ile Thr Val Pro Gly Ala Ala Val Cys Ser Ser Gln Thr Pro
421 85 90 95
424 Cys Pro Ala Tyr Pro Ile Val Ile Tyr Gly Pro Pro Pro Pro Gly Tyr
425 100 105 110
428 Thr Val Gln Pro Gly Glu Tyr Gly Thr Pro Pro Glu Gly Tyr Gly Ala
429 115 120 125
432 Gln Pro Gly Gly Tyr Gly Ala Pro Pro Met Gly Tyr Gly Ala Pro Pro
433 130 135 140
436 Val Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly
437 145 150 155 160
440 Tyr Gly Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly
441 165 170 175
444 Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly Ala Pro
445 180 185 190
448 Pro Ala Gly Tyr Gly Ala Pro Pro Ala Gly Asn Glu Ala Leu Pro Pro
449 195 200 205
452 Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr Ala Ala Ser His Arg Ser
453 210 215 220
456 Met Thr Ala Gln Gln Glu Thr Ser Leu Pro Thr Thr Ser Ser Ser
457 225 230 235
460 <210> SEQ ID NO: 10
462 <211> LENGTH: 225
464 <212> TYPE: PRT
466 <213> ORGANISM: Homo sapiens
470 <400> SEQUENCE: 10
472 Met Pro Phe Asp Leu Met Thr Asn Leu Thr Val Glu Gln Pro Val Phe
473 1 5 10 15
476 Ala Ala Asn Phe Ile Lys Gly Thr Ile Gln Ala Ala Pro Tyr Gly Gly
477 20 25 30
480 Trp Glu Gly Gln Ala Thr Phe Lys Leu Val Phe Arg Asn Gly Asp Ala
481 35 40 45
484 Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Val Ile Val
485 50 55 60
488 Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Pro Gly Tyr Gly
489 65 70 75 80
492 Ala Pro Pro Ala Gly Tyr Gly Ala Gln Pro Val Gly Asn Glu Gly Pro

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/864,291

DATE: 12/11/2001

TIME: 15:07:45

Input Set : A:\1669 0050001 seq list.txt

Output Set: N:\CRF3\12112001\I864291.raw

L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8